

- 1 -

piece 1, NC\_000913, yjiH\_kptA+, config: linear, direction: +, begin: 4558674, end: 4558972

Sequence logo showing the conservation of amino acids at each position of the peptide chain. The sequence starts with fMet and ends with Ala. Positions 1 through 10 are labeled with their respective codons and positions 11 through 20 are labeled with their corresponding amino acids. A red box highlights the C-terminal region (positions 18-20).

{-----} sd-(12)-ir 4558807 Gap 4.0 bits p35 3.9 bits

|-----| sd-ir 4558807 yjiH\_kptA+ total 6.5 bit

5' c g g a a a a a t t a c g c t g t g g a a a a g g o t c t g c g c a g g a t t g a g t t g c a g a a a t t c a t a a a c c a a g t g a c a t g a c a t c a 3'

- - - - - fMet - trp - lys - arg - leu - cys - ala - gly - leu - ser - cys - arg - lys - phe - ile - asn - gln - val - thr - met - thr - ser -

- gly - lys - ile - thr - leu - cys - gly - lys - gly - ser - ala - gln - asp -

- glu - lys - leu - arg - cys - val - glu - lys - ala - leu - arg - arg - ile - glu - leu - gln - lys - ile - his - lys - pro - ser - asp - asn - asp - ile - ser

[###> orf 24 codons

1

• 4

... ----- } p35-(21)-p10 4558846 Gap 3.3 bits

... -----| p35-p10 4558846 total 4.5 bits

55

{-----} sd-(6)-ir 4558908 Gap 4.3 bits

|-----| sd-dir 4558908 |

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{-----| p35-(24)-p10 4558905 Gap 2.4 bits  
|-----| p35-p10 4558905 total 5.6 bits  
{-----| ... p35-(22)-p10 455893
```

5' \*ggtaaaaaaacagaaaaatccaggagacaaacgagatgtccaaacaaatcgaaa 3'

lys

... ir yjiH\_kptA+ 10 3.6 bits [----- ... NC\_000913.kptA

Figure 10. The effect of the number of hidden layers on the performance of the proposed model.

For more information about the study, please contact Dr. Michael J. Hwang at (310) 794-3000 or email at [mhwang@ucla.edu](mailto:mhwang@ucla.edu).

{-----} sd-(12)-in 4558953 Gap 4.0 bits  
{-----} sd-ir 4558953 yjih\_kpta+ total 7.8 bits